

AMENDMENTS TO THE SPECIFICATION

Please add the following new paragraph to page 1 above line 2:

This application is the National Stage of International Application No. PCT/EP03/02629, which claims the benefit under 35 U.S.C. §119(e) of U.S. Provisional Application 60/363,125, filed 03/11/2002.

Please amend the paragraph on page 25 beginning at line 8 to read:

Figure 5 illustrates the genomic organisation of *LpTFL1* and similarity of the deduced protein with other plant PEBPs. (A) The upper bar shows the genomic organisation of the gene, including the untranslated (black boxes) and the translated (white boxes) regions. A 180bp DNA fragment was isolated from ryegrass by RT-PCR. (B) Comparison of the deduced protein sequence for the *LpTFL1* gene (accession no. AF316419) with those of *TFL1* (Bradley et al., 1997; Ohshima et al., 1997), *CEN* (Bradley et al., 1996), *SP* (Pnueli et al., 1998), *BNTFL1-1* and *BNTFL1-3* (Mimida et al., 1999), *CET1*, *CET2*, and *CET4* (Amaya et al., 1999), *FDR1* and *FDR2* (accession nos. AAD42896 and AAD42895, respectively), and *FT* (Kardailsky et al., 1999; Kobayashi et al., 1999). In figure 5(b) the sequences correspond to the sequence listing as follows: TFL1 is SEQ ID NO: 4, BNTFL1-1 is SEQ ID NO: 5, BNTFL1-3 is SEQ ID NO: 6, CEN is SEQ ID NO: 7, CET2 is SEQ ID NO: 8, CET4 is SEQ ID NO: 9, SP is SEQ ID NO: 10, CET1 is SEQ ID NO: 11, LpTFL1 is SEQ ID NO: 3, FDR2 is SEQ ID NO: 12, FDR1 is SEQ ID NO: 13, FT is SEQ ID NO: 14.

CLUSTAL W program was used to make the alignment and the deduced distance tree. Identical residues are in black. Dashed lines indicate gaps introduced by the program to achieve maximum alignment. Identical intron positions among all species are marked with black arrowheads. White arrowheads indicate amino acids identified to be at the ligand-binding sites by crystallography (Banfield and Brady, 2000) and asterisks indicate amino acids in which point mutations were described for Arabidopsis (Bradley et al., 1997; Ohshima et al., 1997) and tomato (Pnueli et al., 1998). (C) Distance tree of different plant PEBPs. The lengths of the horizontal lines are proportional to the similarity between the predicted protein sequences;